The Humungous Fungus of Michigan Three Decades On

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Abstract

In the late 1980s, Smith, Bruhn, and Anderson[1] discovered a genetic individual of the fungus *Armillaria gallica* that extended over 37 hectares of forest floor and encompassed hundreds of tree root systems in Northern Michigan. Based on observed growth rates, the individual was estimated to be at least 1500 years old with a mass of 100,000 kg. The conclusion was that the Michigan individual of *A. gallica* was among the largest and oldest organisms on earth, a remarkable claim given that Armillaria is essentially a microorganism existing largely as microscopic hyphae embedded in their substrate. Nearly three decades on, we returned to the site of the large Michigan individual with the tools of whole-genome sequencing. Here, we show (a) that the large individual is still alive on its original site and (b) that mutation has occurred within the somatic cells of the large individual, reflecting its historical pattern of growth from a

single point. The overall rate of mutation, however, was extremely low. On the spectrum of mutability in somatic cells, Armillaria occupies the extreme of stability, opposite the extreme of instability as typified by cancer[2].

Main

Since the discovery of the Michigan individual[1,3], much has been learned about genomes, gene content, and gene expression in Armillaria. A general picture of how individuals of this fungus become established and persist in woodlands has emerged. Because of its broad host range, capacity for enzyme production, and rhizomorphs, its unique organs of local dispersal, Armillaria appears to be adapted for persistent growth in local habitats[4]. Since its discovery, it is clear that the Michigan individual of *A. gallica* is not unique in its size and age. Any stable, relatively undisturbed forest could support large, old Armillaria individuals. Indeed, at least two others have been reported to exceed the area covered by the Michigan individual[5-7].

Armillaria lives both as a saprophyte on dead wood and as a necrotrophic parasite, killing host plant tissues ahead of the advance of growing mycelia by secreting hydrolytic enzymes and possibly virulence factors[8]. The range of potential host plants is broad encompassing both angiosperm and conifer trees[9]. The large genome size of Armillaria relative to its sister taxa is due to increased gene content, particularly in plant cell wall degrading enzymes, and not to the proliferation of transposable elements [8]. Individuals of Armillaria are established when mating occurs between haploid spores or their germlings[10,11]. After mating, a diploid mycelium is established rather than the dikaryotic mycelium typical of other basidiomycetes. From mycelium, rhizomorphs

develop and push through the soil and decaying woody substrates in much same way as a plant root. Rhizomorphs function as foraging organs in locating new sources of food in dead wood or weakened trees and they can also persist in soil in stasis until new substrates become available. Gene expression in rhizomorph development shares much the same signature of multicellularity found in fruit body development [8]. Rhizomorphs also share a pattern of gene expression underlying enzyme production with vegetative mycelium[8]. Against this background, the focus of this study was on the mutability of Armillaria - detecting genomic change in the spatial record left from the proliferation of somatic cells in space from a single zygote ancestor.

The large individual of *A. gallica* in Michigan was first identified in the late 1980s by making spatially mapped collections of the fungus and then genotyping them over multiple loci[1,3]. We refer to this individual here as C1, corresponding to Clone 1 in the original publication [1] and to "The Humungous Fungus" as named by the news media at the time. All collections of C1 had the same multilocus genotype and shared an identical mitochondrial type. Other nearby individuals had different multilocus genotypes and mitochondrial types[3,12]. Another individual of lesser spatial extent, designated C2 here, was described in addition to C1.

In 2015-2017, we revisited the site of the large individual and made 245 collections linked to GPS coordinates (Supplementary Table 1). Figure 1 shows distribution of isolates representing C1, C2, and all other genotypes, which were excluded here from further analysis.

Fifteen collections of C1 were Illumina sequenced (Supplementary Table 2) to approximately 100X average coverage (NCBI Accession: PRJNA393342). The

sequence reads were initially aligned with a 98 kb mtDNA reference (JGI project number), which was derived from another individual of *A. gallica* from Ontario, Canada[13]; JGI *Armillaria gallica* 21-2 v1). Each of C1, C2, and three additional individuals from the Michigan site had a unique mtDNA genotype based on well-defined SNPs (Supplementary Table 2). The recent Illumina sequenced collections of C1 have the same mtDNA genotype with a living strain of C1 that was collected in the late 1980s. In addition, the recent collections of C2 are linked to a C2 strain from the late 1980s by having the identical mtDNA genotype (Supplementary Table 2).

To test for the signature of mutation, we searched for variation in the nuclear genome of the Illumina sequenced strains. After all filters were applied, 163 variants were found (Supplementary Table 3). In this search, the key requirements for eliminating false calls were to require (a) that candidate sites had at most two alleles among the sequence reads, one reference and one alternate, (b) that one or more strains have 0% or 100% of the reads representing the alternate allele (a "purity" criterion), and (c) that in the heterozygous sites the allele frequencies hovered around 50% (30-70%).

Two general kinds of genetic changes were seen. First, for 151 cases, only single sites experienced the change and adjacent sites in the genome were not affected. We interpret these changes as point mutations resulting in a gain of heterozygosity. The heterozygous strains after mutation had a nearly equal mix of reference and alternate alleles among the Illumina reads, while the homozygous strains had purely one allele. Second, there were regions in strains that were homozygous at a number of adjacent sites that were otherwise heterozygous other strains; we interpret

these events as loss of heterozygosity (LOH) in which a string of adjacent SNP sites that were formerly heterozygous all become homozygous simultaneously, as can happen with mitotic gene conversion. That only six LOH tracts were observed (Supplementary Table 3), and that the preponderance of the original heterozygosity in the individual has been maintained, is remarkable given the potential for mitotic gene conversion and crossing over, which would lead to homozygosity over substantial portions of chromosome arms.

The predominant pattern of both point mutation and LOH was that genetic changes were observed as singletons, present in no more than one Illumina sequenced strain (130 of 163 sites, Supplementary Table 3). As expected for recent mutations mostly unaffected by selection[14], the majority (73%) of point mutations were due to C to T transitions (insert in Supplementary Table 3).

On average, each strain had about 10 singleton changes that were not shared among the other strains. A minority of changes (33 sites), however, were shared among two or more of the strains. These shared changes were particularly informative because they reflect the historical growth pattern of the individual, while the singletons reflect a history of units of the individual persisting in place over time, presumably after the period of general expansion had occurred. This interpretation arises from the fact that individuals of Armillaria cannot exist in stasis over the long term. Existing food sources become exhausted and new sources of food become available, meaning that growth of the fungus is necessary even to remain in the same place.

To examine the spatial relationships of the mutations, we constructed a phylogeny of 14 of the 15 Illumina sequenced isolates of C1 (one strain, no. Ar188, had

lower-than-expected coverage and was excluded from this analysis) using the variants in Supplementary Table 3 as characters and maximum parsimony as the optimality criterion (Fig. 2). The phylogeny shows a high degree of internal consistency and the nesting of the clades in space can be interpreted as reflecting past growth and colonization patterns. Three sites of the 33 sites, however, showed homoplasy in the phylogeny; at these sites, changes occurred two or three times in different branches of the tree. These examples are unlikely due to independent mutation. With a low mutation rate and approximately 100 mb in the genome, the candidate sites for mutation are essentially infinite. The alternative explanation is that the parallel changes could represent single somatic recombination events during the early expansion phase after the individual was established. The potential of fungi for somatic recombination has ample precedent [15,16].

Next, for an independent test of the phylogenetic pattern among Illumina sequenced strains, we tested nine sites in Supplementary Table 3 among all isolates of C1. Once again, the changes showed a nesting pattern in space, with the spatially discrete sectors reflecting their mutational history (Fig. 3). A plausible branching pattern for the mycelium would reflect the phylogeny of nuclei over what is likely several thousands of years of growth by C1.

Despite our ability to identify and map mutant alleles in the Armillaria mycelium, estimating the rate of mutation is problematic because we do not know the number of cell divisions intervening between any two isolates. We can estimate the number of genetic differences among the Illumina sequenced isolates experimentally, but the number of intervening cell divisions is inseparable from the mutation rate (no.

differences = no. cell divisions times the mutation rate). Mutation rates, however, have been estimated in other organisms[17] and we can therefore assume an average mutation rate on the low end of the spectrum, 10^{-10} per base, per cell replication. (Note that mutation rate varies across the genome and among individuals[18].) With a genome of 100 mb, a mutation is expected every 100 cell divisions in a haploid genome and every 50 cell divisions in a diploid genome, such as that of *A. gallica*. The pairs of strains were separated by an average of ca. 20 mutations, even those spatially separated by 1 km, the minimum path of growth separating them. This translates to only 1000 cell divisions over the 1 km, or only one division every 1 m of growth. If we assume a higher mutation rate, then the estimate of one cell division per meter of growth increases even further. Such a dearth of cell division is hard to reconcile with the microscopic size of fungal hyphae.

How might individuals of Armillaria protect themselves from mutation from cell division during growth? We see three possibilities, which are not mutually exclusive. First, the tips of rhizomorphs, which represent the inoculum potential for colonization, may remain relatively quiescent with respect to cell division, much like the apical meristem of plant roots[13,19] and germline cells in mammals[20]. The rhizomorph tip, however, may be propelled forward by cell division and elongation behind the tip. In this way, the rhizomorph tip may minimize cell division even as it moves through its substrate. There is also precedent for avoidance of cell division in the shoots of plants in which axial meristems are derived from apical meristems with remarkably few intervening cell divisions[21]. A second possibility is that repair processes may have been driven to higher efficiency by natural selection up to the point where genetic drift

negates any additional diminishing fitness benefit[22,23]. Also, Armillaria exists in environments that may be of low mutagenic potential. UV radiation, for example, is low in such environments and damage such as pyrimidine dimer formation may be lower than in other environments. The third possibility is that the distribution of DNA strands after replication is asymmetric; cells perpetuating the lineage tend to receive old DNA while cells committed solely to local development and not to perpetuating the lineage receive new DNA[24]. In Armillaria, this would mean that cells in the rhizomorph tip would retain the old DNA, with the subtending cells committed to local, dead-end development would receive the new DNA. The rhizomorphs tips perpetuating the lineage would retain fewer mutations than cells committed to local differentiation and not to perpetuating the lineage. The extent to which each of these mechanisms may contribute to stability remains to be determined.

Here, we followed clonal evolution within cell lineages of a single fungal individual of Armillaria in a spatial context. This follows an earlier analysis of a much smaller Armillaria individual in Ontario[13]. Our picture of clonal evolution in individuals of Armillaria closely parallels that in cancer progression within single individuals[25-28]. Cancer progression, however, is accompanied by extreme genomic instability[2], not necessarily due to loss of function in DNA repair processes, but rather to loss of control of DNA replication; the rate of replication increases to the extent that fidelity suffers and DNA damage accumulates rapidly. Evolution in cancer occurs on a time span shorter than the life span of the individual affected. Evolution occurs similarly in Armillaria individuals, but over a span of centuries and millennia, and is characterized by extreme

genomic stability. The genomic stability of Armillaria and the underlying mechanisms allowing such stability may provide a useful counterpoint to cancer.

Methods Summary

In 2015 – 2017, we made 245 collections of Armillaria linked to GPS coordinates on the site of the large individual of *A. gallica.* DNA was extracted from each of the collections, which were initially genotyped with polymorphic DNA markers and were tested for somatic compatibility with one another in order to identify collections that represent the large individual C1 (110 collections). Fifteen collections of C1 were Illumina sequenced in order to discover genomic variants. The variants were then spatially mapped over the Illumina sequened strains, and, in nine cases, over the 110 collections of the large individual.

Online methods

Sample

In 2015-2017, we revisited the site of the large individual of *A. gallica* and made 245 collections linked to GPS coordinates (Supplementary Table 1). Collections were mostly pure cultures from rhizomorphs, but in the fall of 2015 and of 2016, samples also included fruit-body tissues which were used directly in DNA analysis. Subsequent methods generally followed Anderson and Catona[13].

Culturing and DNA extraction

Rhizomorphs were cut into 2 cm segments and placed in 2.5% hypochlorite bleach for ten minutes to surface disinfect. The rhizomorphs were then trimmed to less than 1 cm and placed on 2% malt-extract agar medium. Liquid cultures were in 2% malt extract without agar. Mycelium was harvested, flash frozen in liquid N2 and then lyophilized.

DNA was extracted with a CTAB- low salt CTAB precipitation method as described earlier[29].

Somatic compatibility testing

To determine whether or not a collection represented C1, we tested for somatic compatibility (Supplementary Table 1), which distinguishes the ability of growing mycelia of the same individual to merge seamlessly in culture and mycelia of different individuals to react with a zone of cell death and pigmentation[30]. We noted one large grouping of 110 isolates that were later confirmed to represent C1 and a smaller grouping of eight isolates that matched the C2 described earlier [1,3]. C1 and C2 are still centered on the same respective localities as reported in 1992 [8].

Initial genotyping

Polymorphic molecular markers were also used to test whether a new collection represented the C1 identity or not (Supplementary Table 1). For example, in one segment of DNA, homozygosity for absence of a MboI site has a frequency of 0.64 in the general population [12]. In addition, the 3' end of the 25S rRNA gene is heterozygous in C1 for a length polymorphism, a genotype that has a frequency of 0.21 in the population. The frequency of the combined genotype of the C1 individual over the two DNA regions is 0.13. The combination of the two DNA regions and somatic compatibility drives the probability of a spurious match in a non-C1 individual much lower.

Illumina sequencing

HiSeq Illumina sequencing was by paired-end with 155 bp reads at the Centre for Applied Genomics at the Hospital for Sick Children, Toronto. The Illumina sequences for 15 collections of C1 are deposited as accession PRJNA393342 in the SRA at NCBI.

Bioinformatics

The pipeline mapped the raw fasta files onto the reference genome, produced the pileup files from the resulting Bam files, and then filtered the pileup files to discover the variation among the Illumina sequenced strains. The pipeline is described in detail in Supplementary Bioinformatics 1.

References

1 Smith, M. L., Bruhn, J. N. & Anderson, J. B. The fungus *Armillaria bulbosa* is among the largest and oldest organisms. *Nature* **356**, 428-431, doi:10.1038/356428a0 (1992).

2 Negrini, S., Gorgoulis, V. G. & Halazonetis, T. D. Genomic instability - an evolving hallmark of cancer. *Nature Reviews Molecular Cell Biology* **11**, 220-228, doi:10.1038/nrm2858 (2010).

3 Smith, M. L., Duchesne, L. C., Bruhn, J. N. & Anderson, J. B. Mitochondrial genetics in a natural populations of the plant pathogen Armillaria. *Genetics* **126**, 575-582 (1990).

4 Sipos, G., Anderson, J. & Nagy, L. Armillaria. *Current Biology* **28**, R297-R298 (2018).

5 Shaw, C. G. & Roth, L. F. Persistence and distribution of a clone of *Armillaria mellea* in a Ponderosa Pine forest. *Phytopathology* **66**, 1210-1213 (1976).

6 Anderson, J., Ullrich, R., Roth, L. & Filip, G. Genetic identification of clones of *Armillaria mellea* in coniferous forests in Washington. *Phytopathology* **69**, 1109-1111, doi:10.1094/Phyto-69-1109 (1979).

7 Ferguson, B., Dreisbach, T., Parks, C., Filip, G. & Schmitt, C. Coarse-scale population structure of pathogenic Armillaria species in a mixed-conifer forest in the Blue Mountains of northeast Oregon. *Canadian Journal of Forest Research-Revue Canadienne De Recherche Forestiere* **33**, 612-623, doi:10.1139/x03-065 (2003).

8 Sipos, G. *et al.* Genome expansion and lineage-specific genetic innovations in the forest pathogenic fungi Armillaria (vol 1, pg 1931, 2017). *Nature Ecology & Evolution* **2**, 577-577, doi:10.1038/s41559-018-0469-7 (2018).

9 Shaw, C. G. & Kile, G. A. *Armillaria Root Disease*. (United States Department of Agriculture).

10 Korhonen, K. & Hintikka, V. Cytological evidence for somatic diploidization in dikaryotic cells of *Armillariella mellea*. *Archives of Microbiology* **95**, 187 – 192.

11 Ullrich, R. C. & Anderson, J. B. Sex and diploidy in *Armillaria mellea*. *Experimental Mycology* **2**, 119-129, doi:10.1016/S0147-5975(78)80025-5 (1978).

12 Saville, B. J., Yoell, H. & Anderson, J. B. Genetic exchange and recombination in populations of the root-infecting fungus *Armillaria gallica*. *Molecular Ecology* **5**, 485-497, doi:10.1111/j.1365-294X.1996.tb00341.x (1996).

13 Anderson, J. B. & Catona, S. Genomewide mutation dynamic within a long-lived individual of Armillaria gallica. *Mycologia* **106**, 642-648, doi:10.3852/13-367 (2014).

14 Trivedi, J. *et al.* Fungus Causing White-Nose Syndrome in Bats Accumulates Genetic Variability in North America with No Sign of Recombination. *Msphere* **2**, doi:10.1128/mSphereDirect.00271-17 (2017).

15 Clark, T. A. & Anderson, J. B. Dikaryons of the basidiomycete fungus Schizophyllum commune: Evolution in long-term culture. *Genetics* **167**, 1663-1675, doi:10.1534/genetics.104.027235 (2004).

16 Carvalho, D. B., Smith, M. L. & Anderson, J. B. Genetic exchange between diploid and haploid mycelia of *Armillaria gallica*. *Mycological Research* **99**, 641-647, doi:10.1016/s0953-7562(09)80520-0 (1995).

17 Lynch, M. *et al.* Genetic drift, selection and the evolution of the mutation rate. *Nature Reviews Genetics* **17**, 704-714, doi:10.1038/nrg.2016.104 (2016).

18 Ness, R. W., Morgan, A. D., Vasanthakrishnan, R. B., Colegrave, N. & Keightley, P. D. Extensive de novo mutation rate variation between individuals and across the genome of *Chlamydomonas reinhardtii*. *Genome Research* **25**, 1739-1749, doi:10.1101/gr.191494.115 (2015).

19 Aanen, D. Vol. 346 922-923 (Science, 2014).

20 Milholland, B. *et al.* Differences between germline and somatic mutation rates in humans and mice. *Nature Communications* **8**, doi:10.1038/ncomms15183 (2017).

21 Burian, A., de Reuille, P. B. & Kuhlemeier, C. Patterns of Stem Cell Divisions Contribute to Plant Longevity. *Current Biology* **26**, 1385-1394, doi:10.1016/j.cub.2016.03.067 (2016).

22 Lynch, M. Evolution of the mutation rate. *Trends Genet* **26**, 345-352, doi:10.1016/j.tig.2010.05.003 (2010).

23 Lynch, M. The lower bound to the evolution of mutation rates. *Genome Biol Evol* **3**, 1107-1118, doi:10.1093/gbe/evr066 (2011).

24 Aanen, D. K. & Debets, A. J. M. (BioRxiv, 2018).

25 Brown, D. *et al.* Phylogenetic analysis of metastatic progression in breast cancer using somatic mutations and copy number aberrations (vol 8, 14944, 2017). *Nature Communications* **8**, doi:10.1038/ncomms15759 (2017).

26 Crespi, B. & Summers, K. Evolutionary biology of cancer. *Trends in Ecology & Evolution* **20**, 545-552, doi:10.1016/j.tree.2005.07.007 (2005).

27 Navin, N. E. & Hicks, J. Tracing the tumor lineage. *Molecular Oncology* **4**, 267-283, doi:10.1016/j.molonc.2010.04.010 (2010).

28 Sprouffske, K., Merlo, L. M. F., Gerrish, P. J., Maley, C. C. & Sniegowski, P. D. Cancer in light of experimental evolution. *Current Biology* **22**, R762-R771, doi:10.1016/j.cub.2012.06.065 (2012).

29 Smith, M. L., Bruhn, J. N. & Anderson, J. B. Relatedness and spatial distribution of Armillaria genets infecting red pine seedlings. *Phytopathology* **84**, 822-829, doi:10.1094/Phyto-84-822 (1994).
30 Worrall, J. J. Somatic incompatibility in basidiomycetes. *Mycologia* **89**, 24-36, doi:10.2307/3761169 (1997).

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Contributions

J.N.B., J.B.A., and M.L.S. planned the study and did the field collecting. D.K. did the laboratory culturing and somatic compatibility tests, DNA extractions, PCR, Sanger sequencing, and preparation of DNA for Illumina sequencing. N.R. and H.W. did the bioinformatic analysis of the Illumina sequences and subsequent nuclear SNP

discovery. J.B.A. did the analysis of mtDNA variation. J.N.B., J.B.A., and M.L.S. wrote the paper with input from D.K., N.R., and H.W.

Competing interests

The authors declare no competing financial interests.

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Supplementary Information

Bioinformatics 1

Supplementary Table 1

Supplementary Table 2

Supplementary Table 3

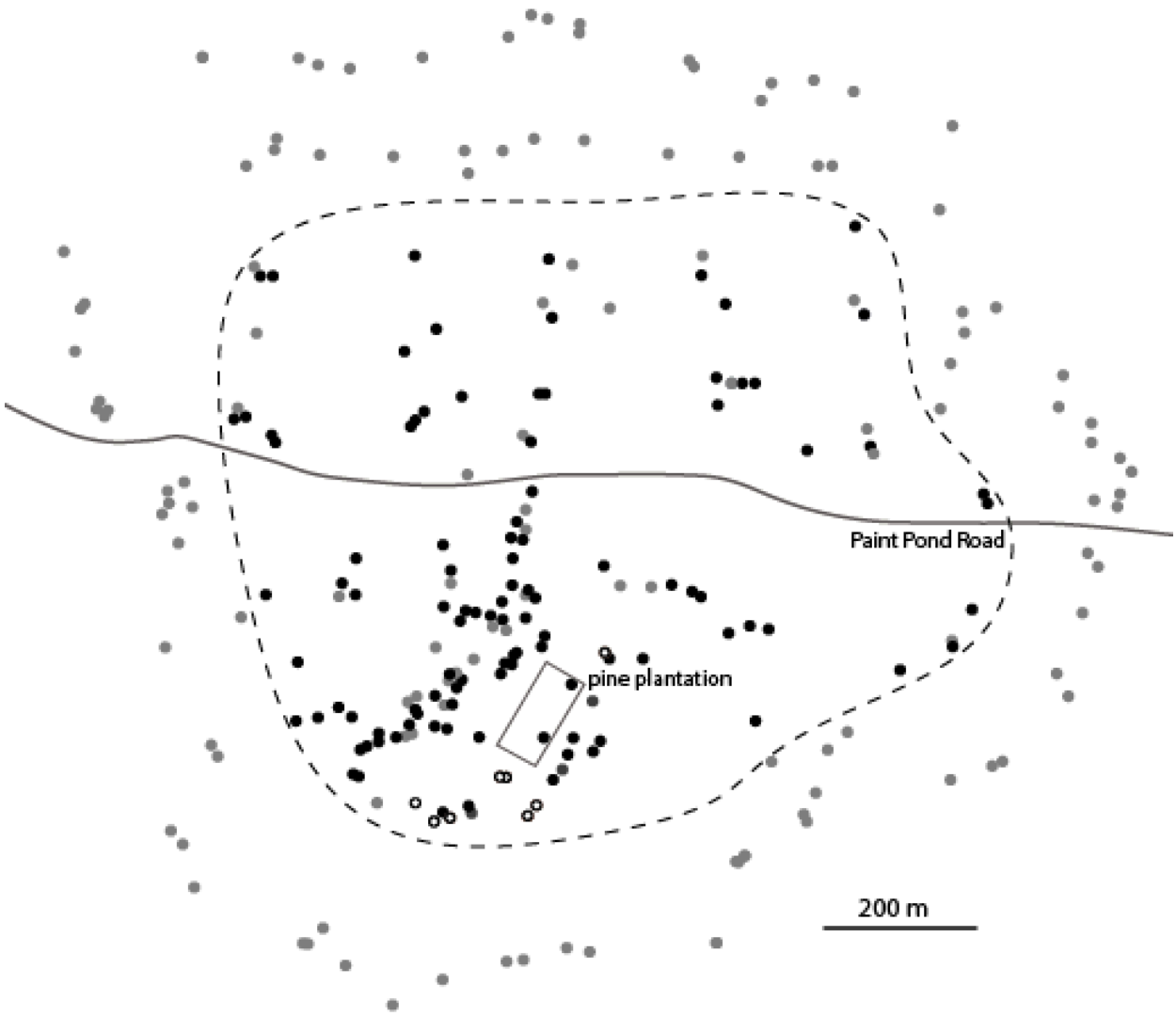

Figure 1. Map of all collections of Armillaria. Back dots, C1; open circles, C2; gray dots, all other individual combined. The outline of the pine plantation and Paint Pond Road are included as alignment features. The dashed line encompasses collections of C1 (and includes some non C1 collections.

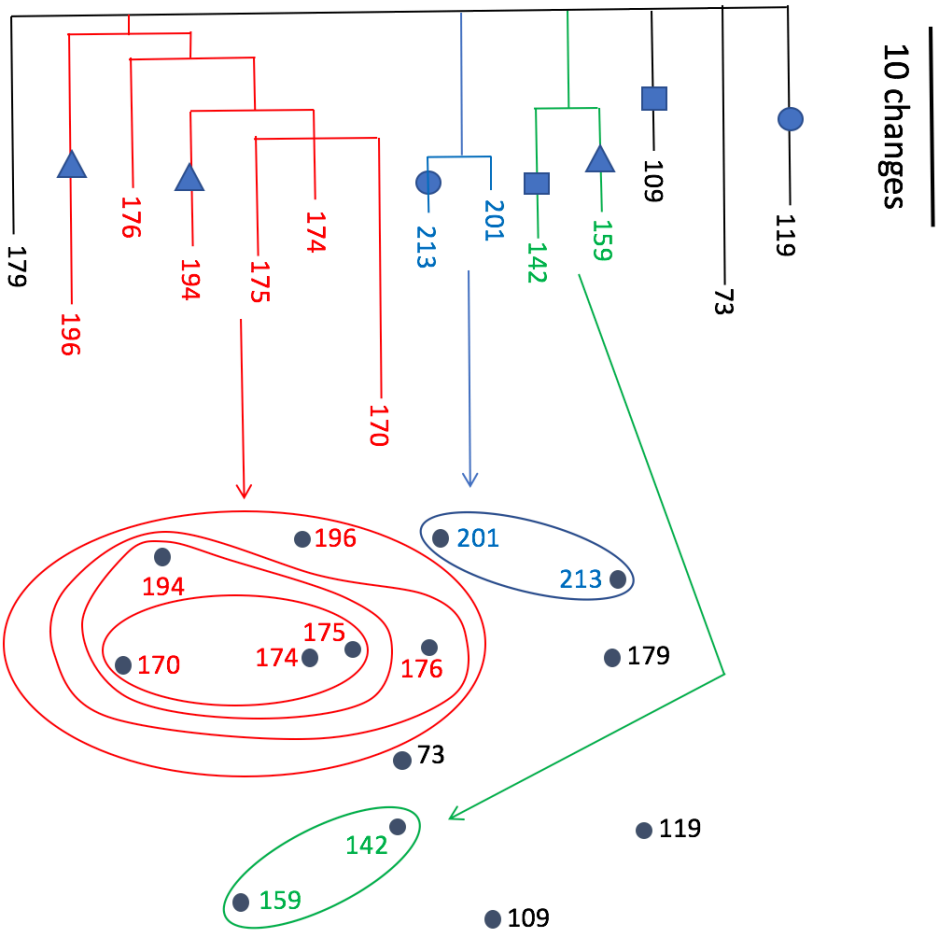

Figure 2. Phylogeny of Illumina sequenced strains of *A. gallica* tied to spatial origin. The variants for this geophylogeny are listed in Supplementary Table 3. Symbols represent sites at which changes occur in different parts of the tree due either to recurrent mutation (unlikely) or recombination. Circles, contig 12, position 174630; squares, contig 61, position 336513, triangles, contig 33, position 701686 (Supplementary Table S).

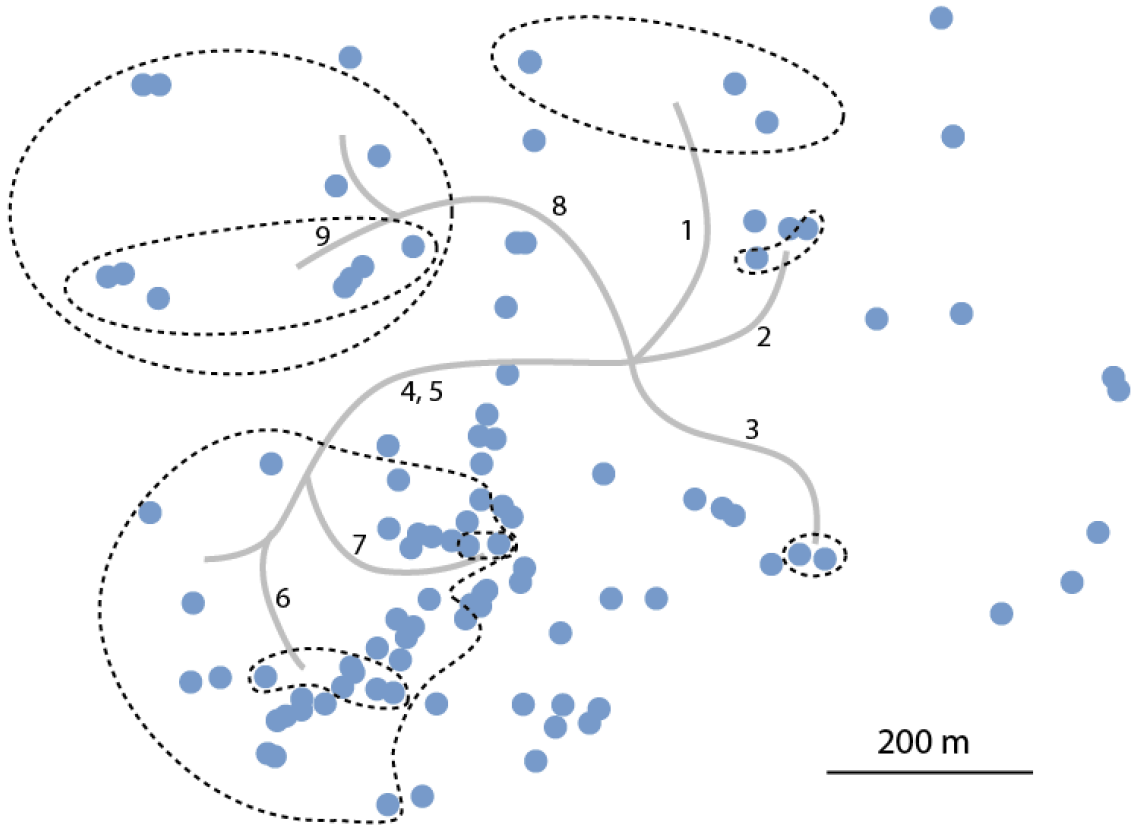

Figure 3. Variation at eight selected genomic sites mapped on all isolates of C1. The sites (list here) were identified from the Illumina sequenced strains in Supplementary Table 1. The sites were then PCR amplified and Sanger sequenced in the other C1 isolates. Site variation is mapped to branches in the phylogenetic tree and spatial sectors encompassing derived genotypes are delineated with dashed lines. Site no. 1, scaffold 8, position 1611588; site no. 2, sc 24, pos 198035; site no. 3, sc 85, pos 12187; site no. 4 sc9, pos 1017767, site no. 5, sc 1, pos 1829026; site no. 6, sc 41, 509147; site no. 7, sc 23, pos 681486; site no. 8, sc 1, pos 1019568; site no. 9 sc 2, pos 3135125 (Supplementary Table 3).